WHAT IS CLAIMED IS:

1. An isolated polynucleotide encoding a polypeptide having a sequence of at least 10 and no more than 500 amino acids, wherein said sequence is derived from the amino acid sequences of SEQ ID NO: 2, 4 or 6.

2. The isolated polynucleotide of claim 1, wherein said sequence is as set forth in amino acid coordinates 490-723 of SEQ ID NO: 2.

3. The isolated polynucleotide of claim 1, wherein said sequence is as set forth in amino acid coordinates 647-723 of SEQ ID NO: 2.

4. The isolated polynucleotide of claim 1, wherein said sequence is as set forth in amino acid coordinates 647-665 of SEQ ID NO: 2.

5. The isolated polynucleotide of claim 1, wherein said sequence is as set forth in amino acid coordinates 647-667 of SEQ ID NO: 2.

6. The isolated polynucleotide of claim 2, wherein said sequence said polypeptide is encoded by nucleotide coordinates 1556-2255 of SEQ ID NO: 1.

7. The isolated polynucleotide of claim 3, wherein said sequence of said polypeptide is encoded by nucleotide coordinates 2025-2255 of SEQ ID NO: 1.

8. The isolated polynucleotide of claim 4, wherein said sequence of said polypeptide is encoded by nucleotide coordinates 2025-2079 of SEQ ID NO: 1.

9. The isolated polynucleotide of claim 5, wherein said sequence of said polypeptide is encoded by nucleotide coordinates 2019-2088 of SEQ ID NO: 1.

10. A nucleic acid construct comprising the isolated polynucleotide of claim 1.

11. The nucleic acid construct of claim 10, further comprising a promoter for regulating transcription of the isolated polynucleotide in sense or antisense orientation.

12. The nucleic acid construct of claim 10, further comprising a positive and a negative selection markers for selecting for homologous recombination events.

13. A host cell comprising the nucleic acid construct of claim 10.

14. An isolated polynucleotide as set forth in SEQ ID NO: 38, 39 or 40.

15. An isolated polypeptide comprising an amino acid sequence of at least 10 and no more than 500 amino acids, wherein said amino acid sequence is derived from SEQ ID NO: 2, 4 or 6.

16. The isolated polypeptide of claim 15, wherein said amino acid sequence is as set forth in SEQ ID NO: 7, 8, 37 or 51.

17. The isolated polypeptide of claim 15, wherein said amino acid sequence is as set forth in amino acid coordinates 490-723 of SEQ ID NO: 2.

18. The isolated polypeptide of claim 15, wherein said amino acid sequence is as set forth in amino acid coordinates 647-723 of SEQ ID NO: 2.

19. The isolated polypeptide of claim 15, wherein said amino acid sequence is as set forth in amino acid coordinates 647-665 of SEQ ID NO: 2.

20. The isolated polypeptide of claim 15, wherein said amino acid sequence is as set forth in amino acid coordinates 647-667 of SEQ ID NO: 2.

21. The isolated polypeptide of claim 17, wherein said amino acid sequence is encoded by nucleotide coordinates 1556-2255 of SEQ ID NO: 1.

22. The isolated polypeptide of claim 18, wherein said amino acid sequence is encoded by nucleotide coordinates 2025-2255 of SEQ ID NO: 1.

23. The isolated polypeptide of claim 19, wherein said amino acid sequence is encoded by nucleotide coordinates 2025-2079 of SEQ ID NO: 1.

24. The isolated polypeptide of claim 20, wherein said amino acid sequence is encoded by nucleotide coordinates 2019-2088 of SEQ ID NO: 1.

25. An antibody or an antibody fragment being capable of specifically binding a polypeptide at least 90 % homologous to SEQ ID NO: 2, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where the gap creation equals 8 and gap extension penalty equals 2.

26. The antibody or antibody fragment of claim 25, wherein said polypeptide is as set forth in SEQ ID NO: 2, 4 or 6.

27. A display library comprising a plurality of display vehicles each displaying at least 6 consecutive amino acids derived from a polypeptide at least 90 % homologous to SEQ ID NOs: 2 as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap creation penalty equals 8 and gap extension penalty equals 2.

28. An oligonucleotide specifically hybridizable with a nucleic acid sequence as set forth in SEQ ID NO: 1.

29. The oligonucleotide of claim 28, wherein said oligonucleotide is a single or double stranded.

30. The oligonucleotide of claim 28, wherein said oligonucleotide is at least 10 bases long.

31. The oligonucleotide of claim 28, wherein said oligonucleotide is hybridizable in either sense or antisense orientation.

32. A pharmaceutical composition comprising a therapeutically effective amount of at least an active portion of a polypeptide being at least 90 % homologous to SEQ ID NO: 2, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where the gap creation equals 8 and gap extension penalty equals 2 or an active portion thereof and a pharmaceutically acceptable carrier or diluent.

33. The pharmaceutical composition of claim 32, wherein said polypeptide is as set forth in SEQ ID NO: 2, 4 or 6.

34. The pharmaceutical composition of claim 32, wherein said active portion of the polypeptide is as set forth in amino acid coordinates 490-723 of SEQ ID NO: 2.

35. The pharmaceutical composition of claim 32, wherein said active portion of the polypeptide is as set forth in amino acid coordinates 647-723 of SEQ ID NO: 2.

36. The pharmaceutical composition of claim 32, wherein said active portion of the polypeptide is as set forth in amino acid coordinates 647-665 of SEQ ID NO: 2.

37. The pharmaceutical composition of claim 32, wherein said active portion of the polypeptide is as set forth in amino acid coordinates 647-667 of SEQ ID NO: 2.

38. The pharmaceutical composition of claim 34, wherein said active portion of the polypeptide is encoded by nucleotide coordinates 1556-2255 of SEQ ID NO: 1.

39. The pharmaceutical composition of claim 35, wherein said active portion of the polypeptide is encoded by nucleotide coordinates 2025-2255 of SEQ ID NO: 1.

40. The pharmaceutical composition of claim 36, wherein said active portion of the polypeptide is encoded by nucleotide coordinates 2025-2079 of SEQ ID NO: 1.

41. The pharmaceutical composition of claim 37, wherein said active portion of the polypeptide is encoded by nucleotide coordinates 2019-2088 of SEQ ID NO: 1.

42. A method of treating HIV infection in a subject, the method comprising providing to a subject in need thereof a therapeutically effective amount of at least an active portion of a polypeptide being at least 90 % homologous to SEQ ID NO: 2, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where the gap creation equals 8 and gap extension penalty equals 2 or an active portion thereof, to thereby treat the HIV infection in the subject.

43. The method of claim 42, wherein said polypeptide is as set forth in SEQ ID NO: 2, 4 or 6.

44. The method of claim 42, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 490-723 of SEQ ID NO: 2.

45. The method of claim 42, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 647-723 of SEQ ID NO: 2.

46. The method of claim 42, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 647-665 of SEQ ID NO: 2.

47. The method of claim 42, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 647-667 of SEQ ID NO: 2.

48. The method of claim 44, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 1556-2255 of SEQ ID NO: 1.

49. The method of claim 45, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 2025-2255 of SEQ ID NO: 1.

50. The method of claim 46, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 2025-2079 of SEQ ID NO: 1.

51. The method of claim 47, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 2019-2088 of SEQ ID NO: 1.

52. The method of claim 42, wherein said providing is effected by:

(i) administering said polypeptide to the subject; and/or

(ii) administering an expressible polynucleotide encoding said polypeptide to the subject.

53. The method of claim 42, further comprising providing to the subject a therapeutically effective amount of Tsg101.

54. A nucleic acid construct system comprising:

(a) a first nucleic acid construct including a first polynucleotide encoding at least an active portion of a polypeptide being at least 90 % homologous to SEQ ID NO: 2, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where the gap creation equals 8 and gap extension penalty equals 2; and

(b) a second nucleic acid construct including a second polynucleotide encoding Tsg101 or an active portion thereof.

55. The nucleic acid construct system of claim 54, wherein said polypeptide is as set forth in SEQ ID NO: 2, 4 or 6.

56. The nucleic acid construct system of claim 54, wherein said first polynucleotide is at least 85 % identical to SEQ ID NO: 1, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap weight equals 50, length weight equals 3, average match equals 10 and average mismatch equals -9.

57. The nucleic acid construct system of claim 54, wherein said first polynucleotide is as set forth in SEQ ID NO: 1, 3 or 5.

58. The nucleic acid construct system of claim 54, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 490-723 of SEQ ID NO: 2.

59. The nucleic acid construct system of claim 54, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 647-723 of SEQ ID NO: 2.

60. The nucleic acid construct system of claim 54, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 647-665 of SEQ ID NO: 2.

61. The nucleic acid construct system of claim 54, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 647-667 of SEQ ID NO: 2.

62. The nucleic acid construct system of claim 58, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 1556-2255 of SEQ ID NO: 1.

63. The nucleic acid construct system of claim 59, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 2025-2255 of SEQ ID NO: 1.

64. The nucleic acid construct system of claim 60, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 2025-2079 of SEQ ID NO: 1.

65. The nucleic acid construct system of claim 61, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 2019-2088 of SEQ ID NO: 1.

66. The nucleic acid construct system of claim 54, wherein each of said first and second nucleic acid constructs further include a promoter for regulating transcription of said first and second polynucleotides in sense or antisense orientation.

67. The nucleic acid construct system of claim 66, wherein said promoter is active in a mammalian cell.

68. A nucleic acid construct comprising a first polynucleotide encoding at least an active portion of a polypeptide being at least 90 % homologous to SEQ ID NO: 2, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where the gap creation equals 8 and gap extension penalty equals 2 and a second polynucleotide encoding Tsg101.

69. The nucleic acid construct of claim 68, wherein said polypeptide is as set forth in SEQ ID NO: 2, 4 or 6.

70. The nucleic acid construct system of 36, wherein said first polynucleotide is at least 85% identical to SEQ ID NO: 1, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where gap weight equals 50, length weight equals 3, average match equals 10 and average mismatch equals -9.

71. The nucleic acid construct of claim 68, wherein said first polynucleotide is as set forth in SEQ ID NO: 1, 3 or 5.

72. The nucleic acid construct of claim 68, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 490-723 of SEQ ID NO: 2.

73. The nucleic acid construct of claim 68, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 647-723 of SEQ ID NO: 2.

74. The nucleic acid construct of claim 68, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 647-667 of SEQ ID NO: 2.

75. The nucleic acid construct of claim 68, wherein said active portion of said polypeptide is as set forth in amino acid coordinates 647-665 of SEQ ID NO: 2.

76. The nucleic acid construct of claim 72, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 1556-2255 of SEQ ID NO: 1.

77. The nucleic acid construct of claim 73, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 2025-2255 of SEQ ID NO: 1.

78. The nucleic acid construct of claim 75, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 2025-2079 of SEQ ID NO: 1.

79. The nucleic acid construct of claim 74, wherein said active portion of said polypeptide is encoded by nucleotide coordinates 2019-2088 of SEQ ID NO: 1.

80. The nucleic acid construct of claim 68, further comprises a promoter for regulating transcription of said first and second polynucleotides in sense or antisense orientation.

81. The nucleic acid construct of claim 80, wherein said promoter is active in a mammalian cell.

82. A method of treating HIV infection and/or a hyperproliferative disease associated with disregulated activity of Tsg101 in a subject, the method comprises downregulating in a subject in need thereof a polypeptide being at least 90 % homologous to SEQ ID NO: 2, as determined using the BestFit software of the Wisconsin sequence analysis package, utilizing the Smith and Waterman algorithm, where the gap creation equals 8 and gap extension penalty equals 2, to thereby treat the HIV infection in the subject.

83. The method of claim 82, wherein said downregulating is effected by downregulating a polynucleotide encoding said polypeptide.

84. The method of claim 83, wherein said downregulating said polynucleotide is effected using a ribozyme being specifically hybridizable with said polynucleotide.

85. The method of claim 83, wherein said downregulating said polynucleotide is effected using an antisense being specifically hybridizable with said polynucleotide.

86. The method of claim 83, wherein said downregulating said polynucleotide is effected using a small interfering RNA duplex being specifically hybridizable with said polynucleotide.

87. The method of claim 86, wherein said small interfering RNA duplex is set forth in SEQ ID NOs: 45 and 46.

88. The method of claim 87, wherein said small interfering RNA duplex is set forth in SEQ ID NOs: 47 and 48.

89. The method of claim 83, wherein said downregulating said polypeptide is effected using an antibody.